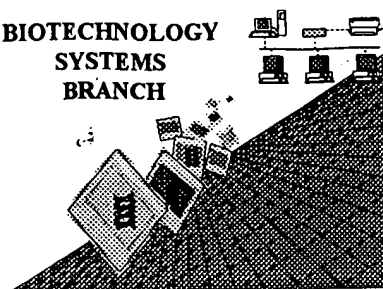


3420

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/992,095

Source: OIPE

Date Processed by STIC: 12/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/992,095

TIME: 12:04:48

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\12052001\I992095.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Benjanin, Stephane
 4 Tanaka, Hiroaki
 6 <120> TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 8 <130> FILE REFERENCE: 91.US5.DIV
 10 <140> CURRENT APPLICATION NUMBER: US/09/992,095
 11 <141> CURRENT FILING DATE: 2001-11-13
 13 <150> PRIOR APPLICATION NUMBER: US 09/924,340
 14 <151> PRIOR FILING DATE: 2001-08-06
 16 <150> PRIOR APPLICATION NUMBER: PCT/IB01/01715
 17 <151> PRIOR FILING DATE: 2001-08-06
 19 <150> PRIOR APPLICATION NUMBER: US 60/305,456
 20 <151> PRIOR FILING DATE: 2001-07-13
 22 <150> PRIOR APPLICATION NUMBER: US 60/302,277
 23 <151> PRIOR FILING DATE: 2001-06-29
 25 <160> NUMBER OF SEQ ID NOS: 112
 27 <170> SOFTWARE: JPatent

ERRORED SEQUENCES

6596 <210> SEQ ID NO: 112
 6597 <211> LENGTH: 387
 6598 <212> TYPE: PRT
 6599 <213> ORGANISM: Homo sapiens
 6601 <400> SEQUENCE: 112
 6602 Met Ser Thr Phe Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro
 6603 1 5 10 15
 6604 Thr Val Leu Cys Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly
 6605 20 25 30
 6606 Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys
 6607 35 40 45
 6608 Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
 6609 50 55 60
 6610 Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val
 6611 65 70 75 80
 6612 Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His
 6613 85 90 95
 6614 Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly
 6615 100 105 110
 6616 Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys
 6617 115 120 125
 6618 Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln
 6619 130 135 140
 6620 Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly
 6621 145 150 155 160
 6622 Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp
 6623 165 170 175

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/992,095

DATE: 12/05/2001

TIME: 12:04:50

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\12052001\I992095.raw

```

6624 Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn
6625           180           185           190
6626 Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg
6627           195           200           205
6628 Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala
6629           210           215           220
6630 Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr
6631           225           230           235           240
6632 Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys
6633           245           250           255
6634 Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr
6635           260           265           270
6636 Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro
6637           275           280           285
6638 Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg
6639           290           295           300
6640 Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro
6641           305           310           315           320
6642 Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala
6643           325           330           335
6644 Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His
6645           340           345           350
6646 Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly
6647           355           360           365
6648 Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys
6649           370           375           380
6650 Lys Ala Pro
6651           385

```

E--> 6652 ¹⁷ deletesee next page

<210> 30
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>

<221> UNSURE

<222> 49 Xaa is at location 29 (a positive (+) 29)

<223> Xaa = Glu, *

Xaa can only represent a single amino acid, not a stop codon or gap in the sequence

<400> 30

Met	Gly	Arg	Thr	Arg	Glu	Ala	Gly	Cys	Val	Ala	Ala	Gly	Val	Val	Ile
-20					-15					-10					-5
Gly	Ala	Gly	Ala	Cys	Tyr	Cys	Val	Tyr	Arg	Leu	Ala	Trp	Gly	Arg	Asp
			1				5					10			
Glu	Asn	Glu	Lys	Ile	Trp	Asp	Glu	Asp	Glu	Glu	Ser	Thr	Asp	Thr	Ser
	15					20					25				
Xaa	Ile	Gly	Val	Glu	Thr	Val	Lys	Gly	Ala	Lys	Thr	Asn	Ala	Gly	Ala
30						35					40				
Gly	Ser	Gly	Ala	Lys	Leu	Gln	Gly	Asp	Ser	Glu	Val	Lys	Pro	Glu	Val
45					50					55				60	
Ser	Leu	Gly	Leu	Glu	Asp	Cys	Pro	Gly	Val	Lys	Glu	Lys	Ala	His	Ser
			65						70					75	
Gly	Ser	His	Ser	Gly	Gly	Gly	Leu	Glu	Ala	Lys	Ala	Lys	Ala	Leu	Phe
		80					85					90			
Asn	Thr	Leu	Lys	Glu	Gln	Ala	Ser	Ala	Lys	Ala	Gly	Lys	Gly	Ala	Arg
	95						100					105			
Val	Gly	Thr	Ile	Ser	Gly	Asn	Arg	Thr	Leu	Ala	Pro	Ser	Leu	Pro	Cys
110						115					120				
Pro	Gly	Gly	Arg	Gly	Gly	Cys	His	Pro	Thr	Arg	Ser	Gly	Ser	Arg	
125					130					135				140	
Ala	Gly	Gly	Arg	Ala	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Ala	Arg	Ser	Lys
				145						150				155	
Ser	Thr	Arg	Ala	Pro	Ala	Thr	Thr	Trp	Pro	Val	Arg	Arg	Gly	Lys	Phe
			160					165					170		
Asn	Phe	Pro	Tyr	Lys	Ile	Asp	Asp	Ile	Leu	Ser	Ala	Pro	Asp	Leu	Gln
	175					180						185			
Lys	Val	Leu	Asn	Ile	Leu	Glu	Arg	Thr	Asn	Asp	Pro	Phe	Ile	Gln	Glu
190						195					200				
Val	Ala	Leu	Val	Thr	Leu	Gly	Asn	Asn	Ala	Ala	Tyr	Ser	Phe	Asn	Gln
205					210					215				220	
Asn	Ala	Ile	Arg	Glu	Leu	Gly	Gly	Val	Pro	Ile	Ile	Ala	Lys	Lys	Lys
				225						230				235	
Lys	Lys														

"49" denotes a positive 49, not the 49th position in the sequence, when the sequence includes negative numbers

e.g. if the Xaa were in the second position in the sequence the <222> region would be -19

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

Please correct an identical error in sequence 72.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/992,095

DATE: 12/05/2001

TIME: 12:04:51

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\12052001\I992095.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:1471 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1492 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1538 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1593 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:4090 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:71
L:4090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:4157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:6652 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:112